



39754-0611 US.txt

SEQUENCE LISTING

<110> Walker, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> 39754-0611-1CP1CP

<140> 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> 08/594,809

<151> 1996-01-31

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> 622)..(624)

<223> This is the codon for the substituted amino acids of the mutated sequence.

<400> 1

aacatgaaca	tcaaaggatc	gccatggaaa	gggtccctcc	tgctgctgct
ggtgtcaaac	60			
ctgctgctgt	gccagagcgt	ggcccccttg	cccatctgtc	ccggcggggc
tgcccgatgc	120			
caggtgaccc	ttcgagacct	gtttgaccgc	gccgtcgtcc	tgtcccacta
catccataac	180			
ctctcctcag	aaatgttcag	cgaattcgat	aaacggtata	cccatggccg
ggggttcatt	240			
accaaggcca	tcaacagctg	ccacacttct	tcccttgcca	ccccgaaga
caaggagcaa	300			
gccaacaga	tgaatcaaaa	agactttctg	agcctgatag	tcagcatatt
gcgatcctgg	360			
aatgagcctc	tgtatcatct	ggtcacggaa	gtacgtggta	tgcaagaagc
cccggaggct	420			
atcctatcca	aagctgtaga	gattgaggag	caaaccaaac	ggcttctaga
gggcatggag	480			
ctgatagtca	gccaggttca	tcctgaaacc	aaagaaaatg	agatctaccc
tgtctggctg	540			
ggacttccat	ccctgcagat	ggctgatgaa	gagtctcgcc	tttctgctta
ttataacctg	600			
ctccactgcc	tacgcaggga	tnnncataaa	atcgacaatt	atctcaagct
cctgaagtgc	660			
cgaatcatcc	acaacaacaa	ctgctaagcc	cacatccatt	tcattctattt
ctgagaaggt	720			
ccttaatgat	ccgttccatt	gcaagcttct	tttagttgta	tctcttttga
atccatgctt	780			
gggtgtaaca	ggtctcctct	taaaaaataa	aaactgactc	gtagagaca
tc	832			

<210> 2

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (208)

<223> Site mutated amino acid residue where the normal codon coding for serine is modified preferably to encode for aspartate or glutamate, most preferably aspartate.

<400>

Asn Gly 1	Met Ser	Asn Leu	Ile Leu 15	Lys Leu 5	Gly Leu	Ser	Pro	Trp	Lys 10
Leu Val	Val Ala	Ser Pro 30	Asn Leu 20	Leu Pro	Leu Ile	Leu	Cys	Gln 25	Ser
Cys Thr	Pro Leu 45	Gly Arg 35	Gly Asp	Ala Leu	Ala Phe	Arg	Cys 40	Gln	Val
Asp His 60	Arg Asn 50	Ala Leu	Val Ser	Val Ser	Leu Glu	Ser 55	His	Tyr	Ile
Met His 65 75	Phe Gly	Ser Arg	Glu Gly	Phe Phe	Asp Ile 70 80	Lys	Arg	Tyr	Thr
Thr Ser	Lys Leu	Ala Ala	Ile Thr 95	Asn Pro 85	Ser Glu	Cys	His	Thr	Ser 90
Asp Lys	Lys Asp	Glu Phe 110	Gln Leu 100	Ala Ser	Gln Leu	Gln	Met	Asn 105	Gln
Ile Pro	Val Leu 125	Ser Tyr 115	Ile His	Leu Leu	Arg Val	Ser	Trp 120	Asn	Glu
Thr Glu 140	Glu Ala 130	Val Ile	Arg Leu	Gly Ser	Met Lys	Gln 135	Glu	Ala	Pro
Ala Leu 145	Val Leu	Glu Glu	Ile Gly	Glu Met	Glu Glu 150	Gln	Thr	Lys	Arg

155

Leu	Ile	Val	Ser	Gln	Val	His	Pro	Glu	Thr
Lys	Glu	Asn	Glu	Ile	Tyr				170

175

Pro	Val	Trp	Ser	Gly	Leu	Pro	Ser	Leu	Gln
Met	Ala	Asp	Glu	Glu	Ser			185	

190

Arg	Leu	Ser	Ala	Tyr	Tyr	Asn	Leu	Leu	His
Cys	Leu	Arg	Arg	Asp	Xaa		200		

205

His	Lys	Ile	Asp	Asn	Tyr	Leu	Lys	Leu	Leu
Lys	Cys	Arg	Ile	Ile	His	215			

220

Asn	Asn	Asn	Cys
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225

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence is a primer.

<400> 3
gcagggatga ccacaagggtt gac 23

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence is a primer.

<220>
<221> variation
<222> (12)
<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 4
cgcaagggat gnacacaagg ttga 24

<210> 5
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence is a primer.

<220>
<221> variation
<222> (12)
<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 5
acgcagggat gnkataaaat cg 22

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence is a primer.

<400> 6
cgtggccccc atatgttgcc catctg 26